(I) Z_1~Z_2-X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-Z_3~Z_4

or a pharmaceutically-acceptable salt thereof, wherein:

Z_1 is R-C(O)-NR- or RRN-;

Z_2 is an optional 1 to 5 residue peptide or peptide analog;

X_1 is any amino acid residue;

X_2 is any amino acid residue;

X_3 is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X_4 is any amino acid residue;

X_5 is a hydrophobic residue or Gly;

X_6 is a hydrophobic or a hydrophilic residue;

X_7 is Gly, an amide-substituted polar residue or a hydrophobic residue;

X_8 is any amino acid residue;

X_9 is an aliphatic residue;

X_{10} is any amino acid residue;

Z_3 is an optional 1 to 5 residue peptide or peptide analog;

Z_4 is –C(O)OR or –C(O)NRR;

each R is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" represents a bond.

A1

Substitute the following for claim 4:

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4. (once amended) The compound of claim 1 wherein the mimic comprises a mimic of a chaperone G_1 beta-strand with at least two alternating hydrophobic amino acid residues which exhibits antibacterial activity against a Gram-negative bacterium.

A2

Substitute the following for claim 8:

8. (once amended) The compound of claim 1 wherein the mimic comprises a mimic of an amino terminal motif of a pilus subunit selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Substitute the following from claim 12:

12. (once amended) The compound of claim 1 which is a 10-20 residue peptide or peptide analog according to formula (I):

(I) Z_1~Z_2-X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-Z_3~Z_4

or a pharmaceutically-acceptable salt thereof, wherein:

Z_1 is R-C(O)-NR- or RRN-;

Z_2 is an optional 1 to 5 residue peptide or peptide analog;

X_1 is any amino acid residue;

X_2 is any amino acid residue;

X_3 is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X_4 is any amino acid residue;

X_5 is a hydrophobic residue or Gly;

X_6 is a hydrophobic or a hydrophilic residue;

X_7 is Gly, an amide-substituted polar residue or a hydrophobic residue;

X_8 is any amino acid residue;

X_9 is an aliphatic residue;

X_{10} is any amino acid residue;

Z_3 is an optional 1 to 5 residue peptide or peptide analog;

Z_4 is –C(O)OR or –C(O)NRR;

each R is independently hydrogen, ©$_1$C$_6$) alkyl, ©$_2$-C$_6$) alkenyl, ©$_2$-C$_6$) alkynyl or ©$_6$-C$_{14}$) aryl;

each "–" between residues X_1 through X_{10}, Z_2 and X_1 and X_{10} and Z_3 independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" represents a bond.

Substitute the following for claim 14:

14. (once amended) The compound of claim 13 which is selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Please cancel claims 3, 18 and 22-135.

In the Drawings:

Please replace the drawings originally submitted with the formal drawings enclosed.